

Serial Number: 09/910,185

**ENTERED**☐ Changed a file from non-ASCII to ASCII☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.☐ Edited a format error in the Current Application Data section, specifically:☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_☐ Added the mandatory heading and subheadings for "Current Application Data".☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.☐ Inserted colons after headings/subheadings. Headings edited included:☒ Deleted extra, invalid, headings used by an applicant, specifically:☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_☐ Inserted mandatory headings, specifically: \_\_\_\_\_☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_☐ Edited identifiers where upper case is used but lower case is required, or vice versa.☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_☐ Other: \_\_\_\_\_

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

#2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/910,185

DATE: 09/12/2001  
TIME: 11:45:24

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\09122001\I910185.raw

6 <110> APPLICANT: C. Frank Bennett  
7 Susan M. Freier  
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3

## EXPRESSION

11 <130> FILE REFERENCE: RTS-0258  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/910,185  
C--> 13 <141> CURRENT FILING DATE: 2001-07-18  
13 <160> NUMBER OF SEQ ID NOS: 90  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 20  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
21 <220> FEATURE:  
23 <223> OTHER INFORMATION: Antisense Oligonucleotide  
25 <400> SEQUENCE: 1 20  
26 tccgtcatcg ctcctcaggg  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 20  
31 <212> TYPE: DNA  
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34 <220> FEATURE:  
36 <223> OTHER INFORMATION: Antisense Oligonucleotide  
38 <400> SEQUENCE: 2 20  
39 atgcattctg cccccaagga  
42 <210> SEQ ID NO: 3  
43 <211> LENGTH: 5055  
44 <212> TYPE: DNA  
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50 <221> NAME/KEY: CDS  
51 <222> LOCATION: (55)...(4845)  
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56 105  
58 gag gcc cag tcc cac agc tcc acg acc act gaa aag aaa aaa gtt gag  
59 Glu Ala Gln Ser His Ser Ser Thr Thr Thr Glu Lys Lys Lys Val Glu  
60 5 10 15  
62 aat tcc ata gtg aag tgc tcc act cga aca gat gtg agc gag aaa gcc 153  
63 Asn Ser Ile Val Lys Cys Ser Thr Arg Thr Asp Val Ser Glu Lys Ala  
64 20 25 30  
66 gtt gcc tcc agc acc act tct aat gag gat gaa agt cct gga cag act 201  
67 Val Ala Ser Ser Thr Thr Ser Asn Glu Asp Glu Ser Pro Gly Gln Thr  
68 35 40 45  
70 tat cac aga gag aga aga aac gca atc act atg cag cca cag aat gtc 249  
71 Tyr His Arg Glu Arg Arg Asn Ala Ile Thr Met Gln Pro Gln Asn Val  
72 50 55 60 65  
74 cag ggg ctc agc aaa gtc agt gag gaa cct tca aca tcg agt gag gag 297

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79 Arg Ala Ser Leu Ile Lys Lys Glu Ile His Gly Ser Leu Pro His Val  
80 85 90 95  
82 gcg gag ccc tct gtg ccg tac cgc ggg acg gtg ttt gcc atg gac ccc 393  
83 Ala Glu Pro Ser Val Pro Tyr Arg Gly Thr Val Phe Ala Met Asp Pro  
84 100 105 110  
86 agg aat ggt tac atg gag ccc cac tac cac cct cct cat ctt ttc cct 441  
87 Arg Asn Gly Tyr Met Glu Pro His Tyr His Pro Pro His Leu Phe Pro  
88 115 120 125  
90 gcc ttc cat cct cct gta cca att gat gcc aga cat cat gag ggc cgt 489  
91 Ala Phe His Pro Pro Val Pro Ile Asp Ala Arg His His Glu Gly Arg  
92 130 135 140 145  
94 tac cat tac gat cca tct ccg att cct cca ttg cat atg act tcc gcc 537  
95 Tyr His Tyr Asp Pro Ser Pro Ile Pro Pro Leu His Met Thr Ser Ala  
96 150 155 160  
98 tta tct agt agc cct acg tat ccg gac ctg ccc ttc att agg atc tcc 585  
99 Leu Ser Ser Ser Pro Thr Tyr Pro Asp Leu Pro Phe Ile Arg Ile Ser  
100 165 170 175  
102 cca cac cgg aac ccc gct gct gct tcc gag tct ccc ttc agc cct cca 633  
103 Pro His Arg Asn Pro Ala Ala Ala Ser Glu Ser Pro Phe Ser Pro Pro  
104 180 185 190  
106 cat ccc tac att aat ccc tac atg gac tat atc cgc tcc ttg cac agc 681  
107 His Pro Tyr Ile Asn Pro Tyr Met Asp Tyr Ile Arg Ser Leu His Ser  
108 195 200 205  
110 agc cca tcg ctc tcc atg atc tca gca acc cgt ggg ctg agc cct aca 729  
111 Ser Pro Ser Leu Ser Met Ile Ser Ala Thr Arg Gly Leu Ser Pro Thr  
112 210 215 220 225  
114 gat gcg ccc cat gca gga gtc agc cca gca gaa tac tat cat cag atg 777  
115 Asp Ala Pro His Ala Gly Val Ser Pro Ala Glu Tyr Tyr His Gln Met  
116 230 235 240  
118 gcc ctg cta act ggc cag cgc agc ccc tat gca gac att att ccc tca 825  
119 Ala Leu Leu Thr Gly Gln Arg Ser Pro Tyr Ala Asp Ile Ile Pro Ser  
120 245 250 255  
122 gct gcc acc gcc ggc acg ggg gcc atc cac atg gaa tat ctt cat gct 873  
123 Ala Ala Thr Ala Gly Thr Gly Ala Ile His Met Glu Tyr Leu His Ala  
124 260 265 270  
126 atg gat agc acc aga ttc tcc agc ccc agg ctg tca gcc agg ccg agc 921  
127 Met Asp Ser Thr Arg Phe Ser Ser Pro Arg Leu Ser Ala Arg Pro Ser  
128 275 280 285  
130 cga aaa cgt aca ctg tcc ata tca cca ctc tcc gat cat agc ttt gac 969  
131 Arg Lys Arg Thr Leu Ser Ile Ser Pro Leu Ser Asp His Ser Phe Asp  
132 290 295 300 305  
134 ctt cag acc atg ata agg acg tct ccc aac tcc ttg gtc acg att ctc 1017  
135 Leu Gln Thr Met Ile Arg Thr Ser Pro Asn Ser Leu Val Thr Ile Leu  
136 310 315 320  
138 aat aat tcc cgt agc agc tct tca gca agt ggc tcc tat ggt cac tta 1065  
139 Asn Asn Ser Arg Ser Ser Ser Ser Ala Ser Gly Ser Tyr Gly His Leu

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143	Ser Ala Ser Ala Ile Ser Pro Ala Leu Ser Phe Thr Tyr Ser Ser Ala							
144		340		345		350		1161
146	ccc gtc tct ctc cac atg cat cag cag atc cta agc cga caa cag agc							
147	Pro Val Ser Leu His Met His Gln Gln Ile Leu Ser Arg Gln Gln Ser							
148		355		360		365		1209
150	tta ggt tca gcc ttt gga cac agc cct cca ctc atc cac cct gcc cca							
151	Leu Gly Ser Ala Phe Gly His Ser Pro Pro Leu Ile His Pro Ala Pro							
152	370		375		380		385	1257
154	act ttt cca aca cag agg cct att cca ggg atc cct acg gtt ctg aac							
155	Thr Phe Pro Thr Gln Arg Pro Ile Pro Gly Ile Pro Thr Val Leu Asn							
156		390		395		400		1305
158	ccc gtc cag gtc agc tcc ggc cct tct gag tcc tca cag aac aag ccc							
159	Pro Val Gln Val Ser Ser Gly Pro Ser Glu Ser Ser Gln Asn Lys Pro							
160		405		410		415		1353
162	acg agt gag tct gca gtg agc agc act ggt gac ccg atg cac aac aag							
163	Thr Ser Glu Ser Ala Val Ser Ser Thr Gly Asp Pro Met His Asn Lys							
164		420		425		430		1401
166	agg tcc aag atc aaa ccc gat gaa gac ctc ccc agc cca ggg gct cgg							
167	Arg Ser Lys Ile Lys Pro Asp Glu Asp Leu Pro Ser Pro Gly Ala Arg							
168		435		440		445		1449
170	ggg cag cag gaa cag ccc gaa gga aca acc ctt gtc aag gag gaa ggg							
171	Gly Gln Gln Glu Gln Pro Glu Gly Thr Thr Leu Val Lys Glu Glu Gly							
172	450		455		460		465	1497
174	gac aaa gat gaa agc aaa cag gag cct gaa gtc atc tat gag aca aac							
175	Asp Lys Asp Glu Ser Lys Gln Glu Pro Glu Val Ile Tyr Glu Thr Asn							
176		470		475		480		1545
178	tgc cac tgg gaa ggc tgc gcg agg gag ttc gac acc caa gag cag ctt							
179	Cys His Trp Glu Gly Cys Ala Arg Glu Phe Asp Thr Gln Glu Gln Leu							
180		485		490		495		1593
182	gtg cac cat ata aat aac gac cat att cat gga gag aag aag gag ttc							
183	Val His His Ile Asn Asn Asp His Ile His Gly Glu Lys Lys Glu Phe							
184		500		505		510		1641
186	gtg tgc agg tgg ctg gac tgc tca aga gag cag aaa ccc ttc aaa gcc							
187	Val Cys Arg Trp Leu Asp Cys Ser Arg Glu Gln Lys Pro Phe Lys Ala							
188		515		520		525		1689
190	cag tat atg ttg gta gtg cat atg aga aga cac acg ggc gag aag cct							
191	Gln Tyr Met Leu Val Val His Met Arg Arg His Thr Gly Glu Lys Pro							
192	530		535		540		545	1737
194	cac aaa tgc act ttt gaa ggt tgc aca aag gcc tac tcg aga cta gaa							
195	His Lys Cys Thr Phe Glu Gly Cys Thr Lys Ala Tyr Ser Arg Leu Glu							
196		550		555		560		1785
198	aac ttg aaa aca cac ttg aga tct cac act gga gag aaa cca tac gtc							
199	Asn Leu Lys Thr His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Val							
200		565		570		575		1833
202	tgt gag cac gaa ggt tgc aac aag gct ttc tca aat gcc tct gat cgc							
203	Cys Glu His Glu Gly Cys Asn Lys Ala Phe Ser Asn Ala Ser Asp Arg							
204		580		585		590		

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207	Ala	Lys	His	Gln	Asn	Arg	Thr	His	Ser	Asn	Glu	Lys	Pro	Tyr	Val	Cys	
208		595					600					605					
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211	Lys	Ile	Pro	Gly	Cys	Thr	Lys	Arg	Tyr	Thr	Asp	Pro	Ser	Ser	Leu	Arg	
212	610					615					620						
214	aaa	cat	gtg	aag	aca	gtg	cat	ggc	cca	gag	gct	cat	gtc	acc	aag	aag	1977
215	Lys	His	Val	Lys	Thr	Val	His	Gly	Pro	Glu	Ala	His	Val	Thr	Lys	Lys	
216						630					635						
218	cag	cga	ggg	gac	atc	cat	cct	cgg	ccg	cca	ccc	ccg	aga	gat	tcc	ggc	2025
219	Gln	Arg	Gly	Asp	Ile	His	Pro	Arg	Pro	Pro	Pro	Pro	Arg	Asp	Ser	Gly	
220						645			650								
222	agc	cat	tca	cag	tcc	agg	tcg	cct	ggc	cga	ccg	act	cag	gga	gcc	ctt	2073
223	Ser	His	Ser	Gln	Ser	Arg	Ser	Pro	Gly	Arg	Pro	Thr	Gln	Gly	Ala	Leu	
224						660			665								
226	ggt	gag	cag	cag	gac	ctc	agc	aac	act	acc	tca	aag	cgg	gaa	gaa	tgc	2121
227	Gly	Glu	Gln	Gln	Asp	Leu	Ser	Asn	Thr	Thr	Ser	Lys	Arg	Glu	Glu	Cys	
228						675			680								
230	ctc	cag	gtg	aaa	acc	gtc	aag	gca	gag	aag	cca	atg	aca	tct	cag	cca	2169
231	Leu	Gln	Val	Lys	Thr	Val	Lys	Ala	Glu	Lys	Pro	Met	Thr	Ser	Gln	Pro	
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234	agc	cct	ggt	ggt	cag	tct	tca	tgc	agc	agc	caa	cag	tcc	ccc	atc	agc	2217
235	Ser	Pro	Gly	Gly	Gln	Ser	Ser	Cys	Ser	Ser	Gln	Gln	Ser	Pro	Ile	Ser	
236						710					715						
238	aac	tat	tcc	aac	agt	ggg	ctc	gag	ctt	cct	ctg	acc	gat	gga	ggt	agt	2265
239	Asn	Tyr	Ser	Asn	Ser	Gly	Leu	Glu	Leu	Pro	Leu	Thr	Asp	Gly	Gly	Ser	
240						725			730								
242	ata	gga	gac	ctc	agt	gcc	atc	gat	gaa	acc	cca	atc	atg	gac	tca	acc	2313
243	Ile	Gly	Asp	Leu	Ser	Ala	Ile	Asp	Glu	Thr	Pro	Ile	Met	Asp	Ser	Thr	
244						740			745								
246	att	tcc	act	gca	acc	aca	gcc	ctt	gct	ttg	caa	gcc	agg	aga	aac	ccg	2361
247	Ile	Ser	Thr	Ala	Thr	Thr	Ala	Leu	Ala	Leu	Gln	Ala	Arg	Arg	Asn	Pro	
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251	Ala	Gly	Thr	Lys	Trp	Met	Glu	His	Val	Lys	Leu	Glu	Arg	Leu	Lys	Gln	
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255	Val	Asn	Gly	Met	Phe	Pro	Arg	Leu	Asn	Pro	Ile	Leu	Pro	Pro	Lys	Ala	
256						790					795						
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259	Pro	Ala	Val	Ser	Pro	Leu	Ile	Gly	Asn	Gly	Thr	Gln	Ser	Asn	Asn	Thr	
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262	tgc	agc	ttg	ggt	ggg	ccc	atg	acg	ctt	ctc	ccg	ggc	aga	agc	gac	ctc	2553
263	Cys	Ser	Leu	Gly	Gly	Pro	Met	Thr	Leu	Leu	Pro	Gly	Arg	Ser	Asp	Leu	
264						820			825								
266	tct	ggg	gtg	gac	gtc	act	atg	ctg	aac	atg	ctc	aac	aga	agg	gac	agc	2601
267	Ser	Gly	Val	Asp	Val	Thr	Met	Leu	Asn	Met	Leu	Asn	Arg	Arg	Asp	Ser	
268						835					840						
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276						870					875				880			
278	gcc	gag	ggc	cgg	cgg	cag	aac	gtg	agc	gtg	gcc	gac	tcc	tac	gac	ccc	2745	
279	Ala	Glu	Gly	Arg	Pro	Gln	Asn	Val	Ser	Val	Ala	Asp	Ser	Tyr	Asp	Pro		
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282	atc	tcc	acc	gac	gcc	tgc	cgc	cgc	tcc	agc	gaa	gcc	agc	cag	agc	gac	2793	
283	Ile	Ser	Thr	Asp	Ala	Ser	Arg	Arg	Ser	Ser	Glu	Ala	Ser	Gln	Ser	Asp		
284						900					905				910			
286	ggc	ctg	ccc	agc	ctg	ctc	agc	ctc	acg	ccc	gcc	cag	cag	tac	cgc	ctc	2841	
287	Gly	Leu	Pro	Ser	Leu	Leu	Ser	Leu	Thr	Pro	Ala	Gln	Gln	Tyr	Arg	Leu		
288						915					920				925			
290	aag	gcc	aag	tac	gcg	gct	gcc	aca	gga	ggg	ccg	ccg	ccg	acg	ccc	ctg	2889	
291	Lys	Ala	Lys	Tyr	Ala	Ala	Ala	Thr	Gly	Gly	Pro	Pro	Pro	Thr	Pro	Leu		
292	930					935					940				945			
294	ccc	aac	atg	gag	agg	atg	agc	ctg	aag	acg	cgc	ctg	gcg	ctg	ctc	ggg	2937	
295	Pro	Asn	Met	Glu	Arg	Met	Ser	Leu	Lys	Thr	Arg	Leu	Ala	Leu	Leu	Gly		
296						950					955				960			
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306	ccg	cac	gat	gcg	ctg	ggc	cac	ggc	gtg	agg	agg	gcc	agc	gac	ccg	gtg	3081	
307	Pro	His	Asp	Ala	Leu	Gly	His	Gly	Val	Arg	Arg	Ala	Ser	Asp	Pro	Val		
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310	cgg	aca	ggc	tcc	gag	ggc	ctg	gcc	ctg	cct	cgt	gtg	ccg	cgc	ttc	agc	3129	
311	Arg	Thr	Gly	Ser	Glu	Gly	Leu	Ala	Leu	Pro	Arg	Val	Pro	Arg	Phe	Ser		
312	1010					1015					1020				1025			
314	agc	ctc	agc	agc	tgc	aac	ccc	ccg	gcg	atg	gcc	acg	tcc	gcg	gag	aag	3177	
315	Ser	Leu	Ser	Ser	Cys	Asn	Pro	Pro	Ala	Met	Ala	Thr	Ser	Ala	Glu	Lys		
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319	Arg	Ser	Leu	Val	Leu	Gln	Asn	Tyr	Thr	Arg	Pro	Glu	Gly	Gly	Gln	Ser		
320						1045					1050				1055			
322	cga	aac	ttc	cac	tgc	tcc	ccc	tgt	cct	ccc	agc	atc	acc	gag	aac	gtc	3273	
323	Arg	Asn	Phe	His	Ser	Ser	Pro	Cys	Pro	Pro	Ser	Ile	Thr	Glu	Asn	Val		
324						1060					1065				1070			
326	acc	ctg	gag	tcc	ctg	acc	atg	gac	gct	gat	gcc	aac	ctg	aac	gat	gag	3321	
327	Thr	Leu	Glu	Ser	Leu	Thr	Met	Asp	Ala	Asp	Ala	Asn	Leu	Asn	Asp	Glu		
328						1075					1080				1085			
330	gat	ttc	ctg	ccg	gac	gac	gtg	gtg	cag	tat	tta	aat	tcc	cag	aac	caa	3369	
331	Asp	Phe	Leu	Pro	Asp	Asp	Val	Val	Gln	Tyr	Leu	Asn	Ser	Gln	Asn	Gln		
332	1090					1095					1100				1105			
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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date